



ONYX1027-DIV1.ST25.txt
SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> Braselmann, Sylvia

<120> Nucleotide Sequences that Encode Phosphatidylinositol-3' Kinase Associated Proteins and Uses Thereof

<130> ONYX1027-DIV1

<140> US 09/687,230

<141> 2000-10-13

<150> US 08/942,008

<151> 1997-10-01

<150> US 60/030,103

<151> 1996-11-01

<160> 3

<170> PatentIn version 3.1

<210> 1

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<212> DNA

<213> Phosphatidylinositol-3' Kinase

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tgggcctggc gcggggggcg ggcaccgggg cccggtcgga c atg ggc aag aag cac 176
Met Gly Lys Lys His
1 5
aag aag cac aag tcg gac aaa cac ctc tac gag gag tat gta gag aag 224
Lys Lys His Lys Ser Asp Lys His Leu Tyr Glu Glu Tyr Val Glu Lys
10 15 20
ccc ttg aag ctg gtc ctc aaa gta gga ggg aac gaa gtc acc gaa ctc 272
Pro Leu Lys Leu Val Leu Lys Val Gly Gly Asn Glu Val Thr Glu Leu
25 30 35
tcc acg ggc agc tcg ggg cac gac tcc agc ctc ttc gaa gac aaa aac 320
Ser Thr Gly Ser Ser Gly His Asp Ser Ser Leu Phe Glu Asp Lys Asn
40 45 50
gat cat gac aaa cac aag gac aga aag cgg aaa aag aga aag aaa gga 368
Asp His Asp Lys His Lys Asp Arg Lys Arg Lys Lys Arg Lys Lys Gly
55 60 65
gag aag cag att cca ggg gaa gaa aag ggg aga aaa cgg aga aga gtt 416
Glu Lys Gln Ile Pro Gly Glu Glu Lys Gly Arg Lys Arg Arg Arg Val
70 75 80 85
aag gag gat aaa aag aag cga gat cga gac cgg gtg gag aat gag gca 464
Lys Glu Asp Lys Lys Lys Arg Asp Arg Asp Arg Val Glu Asn Glu Ala
90 95 100
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Glu Lys Asp Leu Gln Cys His Ala Pro Val Arg Leu Asp Leu Pro Pro
105 110 115
gag aag cct ctc aca agc tct tta gcc aaa caa gaa gaa gta gaa cag 560
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120 125 130
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Thr Pro Leu Gln Glu Ala Leu Asn Gln Leu Met Arg Gln Leu Gln Arg
135 140 145
aaa gat cca agt gct ttc ttt tca ttt cct gtg act gat ttt att gct 656
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150 155 160 165
cct ggc tac tcc atg atc att aaa cac cca atg gat ttt agt acc atg 704
Pro Gly Tyr Ser Met Ile Ile Lys His Pro Met Asp Phe Ser Thr Met
170 175 180
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gag acc att tat tat aaa gct gca aag aag ctg ttg cac tca gga atg 848
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Val	Phe	Asp	Ser	Glu	Glu	Ala	Glu	Ile	Phe	Gln	Lys	Lys	Leu	Asp	Glu	
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acc	acc	aga	ttg	ctc	agg	gaa	ctc	cag	gaa	gcc	cag	aat	gaa	cgt	ttg	1856
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Glu	Lys	Cys	Ile	Leu	Leu	Asn	Lys									
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Phe Glu Asp Lys Asn Asp His Asp Lys His Lys Asp Arg Lys Arg Lys
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Lys Arg Arg Arg Val Lys Glu Asp Lys Lys Lys Arg Asp Arg Asp Arg
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Leu Asp Leu Pro Pro Glu Lys Pro Leu Thr Ser Ser Leu Ala Lys Gln
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Glu Glu Val Glu Gln Thr Pro Leu Gln Glu Ala Leu Asn Gln Leu Met
130 135 140

Arg Gln Leu Gln Arg Lys Asp Pro Ser Ala Phe Phe Ser Phe Pro Val
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Thr Asp Phe Ile Ala Pro Gly Tyr Ser Met Ile Ile Lys His Pro Met
165 170 175

Asp Phe Ser Thr Met Lys Glu Lys Ile Lys Asn Asn Asp Tyr Gln Ser
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Ile Glu Glu Leu Lys Asp Asn Phe Lys Leu Met Cys Thr Asn Ala Met
195 200 205

Ile Tyr Asn Lys Pro Glu Thr Ile Tyr Tyr Lys Ala Ala Lys Lys Leu
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Leu His Ser Gly Met Lys Ile Leu Ser Gln Glu Arg Ile Gln Ser Leu
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Lys Gln Ser Ile Asp Phe Met Ala Asp Leu Gln Lys Thr Arg Lys Gln
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Lys Asp Gly Thr Asp Thr Ser Gln Ser Gly Glu Asp Gly Gly Cys Trp
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Gln Arg Glu Arg Glu Asp Ser Gly Asp Ala Glu Ala His Ala Phe Lys
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Ser Pro Ser Lys Glu Asn Lys Lys Lys Asp Lys Asp Met Leu Glu Asp
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Lys Phe Lys Ser Asn Asn Leu Glu Arg Glu Gln Glu Gln Leu Asp Arg
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Ile Val Lys Glu Ser Gly Gly Lys Leu Thr Arg Arg Leu Val Asn Ser
325 330 335

Gln Cys Glu Phe Glu Arg Arg Lys Pro Asp Gly Thr Thr Thr Leu Gly
340 345 350

Leu Leu His Pro Val Asp Pro Ile Val Gly Glu Pro Gly Tyr Cys Leu
355 360 365

Val Arg Leu Gly Met Thr Thr Gly Arg Leu Gln Ser Gly Val Asn Thr
370 375 380

Leu Gln Gly Phe Lys Glu Asp Lys Arg Asn Lys Val Thr Pro Val Leu
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Tyr Leu Asn Tyr Gly Pro Tyr Ser Ser Tyr Ala Pro His Tyr Asp Ser
405 410 415

Thr Phe Ala Asn Ile Ser Lys Asp Asp Ser Asp Leu Ile Tyr Ser Thr
420 425 430

Tyr Gly Glu Asp Ser Asp Leu Pro Ser Asp Phe Ser Ile His Glu Phe
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Leu Ala Thr Cys Gln Asp Tyr Pro Tyr Val Met Ala Asp Ser Leu Leu
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Asp Val Leu Thr Lys Gly Gly His Ser Arg Thr Leu Gln Glu Met Glu
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Met Ser Leu Pro Glu Asp Glu Gly His Thr Arg Thr Leu Asp Thr Gly
485 490 495

Lys Glu Met Glu Gln Ile Thr Glu Val Glu Pro Pro Gly Arg Leu Asp
500 505 510

Ser Ser Thr Gln Asp Arg Leu Ile Ala Leu Lys Ala Val Thr Asn Phe
515 520 525

Gly Val Pro Val Glu Val Phe Asp Ser Glu Glu Ala Glu Ile Phe Gln
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530

535

540

Lys Lys Leu Asp Glu Thr Thr Arg Leu Leu Arg Glu Leu Gln Glu Ala
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Gln Asn Glu Arg Leu Ser Thr Arg Pro Pro Gly Asn Met Ile Cys Leu
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Leu Gly Pro Ser Ser Glu Lys Cys Ile Leu Leu Asn Lys
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